## WHAT IS CLAIMED IS:

## CallSeq™

- 1. In a computer system, a method of identifying
  2 an unknown base in a sample nucleic acid sequence, said method
  3 comprising the steps of:
- inputting a plurality of probe intensities, each of said probe intensities being associated with a probe on a chip;
- said computer system comparing said plurality of probe intensities wherein each of said plurality of probe intensities is substantially proportional to a probe hybridizing with at least one sequence; and
- calling said unknown base according to said
   comparison of said plurality of probe intensities.
  - The method of claim 1, wherein said at least
     one sequence includes said sample sequence.
  - 3. The method of claim 2, further comprising the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.
  - 4. The method of claim 3, further comprising the step of calling said unknown base as being a base complement of said probe associated with said higher probe intensity if said ratio is greater than a predetermined ratio value.
  - 5. The method of claim 3, wherein said ratio is
     approximately 1.2.
  - 1 6. The method of claim 2, further comprising the step of sorting said plurality of probe intensities.
  - 7. The method of claim 1, wherein said at least one sequence includes said sample sequence and a reference sequence.

- 1 8. The method of claim 7, further comprising the
- 2 step of said computer system comparing probe intensities of a
- 3 probe hybridizing with said sample sequence to probe
- 4 intensities hybridizing with said reference sequence.
- 1 9. The method of claim 7, further comprising the
- step of calculating first ratios of a wild-type probe
- intensity to each probe intensity of a probe hybridizing with
- 4 said reference sequence, wherein said wild-type probe
- intensity is associated with a wild-type probe.
- 1 10. The method of claim 9, further comprising the
- 2 step of calculating second ratios of the highest probe
- intensity of a probe hybridizing with said sample sequence to
- 4 each probe intensity of a probe hybridizing with said sample
- 5 sequence.
- 1 11. The method of claim 10, further comprising the
- 2 step of calculating third ratios of said first ratios to said
- 3 second ratios.
- 1 12. The method of claim 7, further comprising the
- step of comparing neighboring probe intensities of said
- 3 plurality of probe intensities.
- 1 13. The method of claim 7, wherein probe
- 2 intensities of a probe hybridizing with said reference
- 3 sequence are from a plurality of experiments.
- 1 14. The method of claim 13, further comprising the
- 2 step of said computer system comparing probe intensities of a
- 3 probe hybridizing with said sample sequence to statistics
- 4 about said plurality of experiments.
- 1 15. The method of claim 14, wherein said statistics
- 2 include a mean and standard deviation.

- 1 16. The method of claim 13, further comprising the
- step of normalizing said plurality of probe intensities by
- dividing each probe intensity by a sum of related probe
- 4 intensities.
- 1 17. The method of claim 1, further comprising the
- step of subtracting a background intensity from each of said
- 3 plurality of probe intensities.
- 1 18. The method of claim 1, further comprising the
- 2 step of setting a probe intensity equal to a relative small
- 3 positive number if said probe intensity is less than or equal
- 4 to zero.
- 1 19. The method of claim 1, further comprising the
- 2 step of indicating said unknown base is unable to be called if
- 3 said plurality of probe intensities have insufficient
- 4 intensity to call said unknown base.
- 1 20. The method of claim 1, wherein said unknown
- 2 base is called as being A, C, G, or T.

## Pooling Processing

- 1 21. A method of processing first and second nucleic
- 2 acid sequences, comprising the steps of:
- 3 providing a plurality of nucleic acid probes;
- 4 labeling said first nucleic acid sequence with a
- 5 first marker;
- 6 labeling said second nucleic acid sequence with a
- 7 second marker; and
- 8 hybridizing said first and second labeled nucleic
- 9 acid sequences at the same time.
- 1 22. The method of claim 21, wherein said plurality
- of nucleic acid probes are on a chip.

- 1 23. The method of claim 21, further comprising the
- step of fragmenting said first and second nucleic acid
- 3 sequences at the same time.
- 1 24. The method of claim 21, further comprising the
- 2 step of scanning for said first and second markers on said
- 3 chip, said first and second labeled nucleic acid sequences
- 4 being on said chip.
- 1 25. The method of claim 21, wherein said first and
- 2 second markers are fluorescent markers.
- 1 26. The method of claim 25, wherein said first and
- 2 second markers emit light at different wavelengths upon
- 3 excitation.

## ViewSeq™

- 1 27. In a computer system, a method of analyzing a
- 2 plurality of sequences of bases, said plurality of sequences
- including at least one reference sequence and at least one
- sample sequence, the method comprising the steps of:
- displaying said at least one reference sequence in a
- 6 first area on a display device; and
- displaying said at least one sample sequence in a
- 8 second area on said display device;
- whereby a user is capable of visually comparing said
- 10 plurality of sequences.
- 1 28. The method of claim 27, wherein said plurality
- of sequences are monomer strands of DNA or RNA.
- 1 29. The method of claim 27, wherein said bases are
- 2 A, C, G, or T.
- 1 30. The method of claim 27, wherein said at least
- 2 one reference sequence includes a chip wild-type that has been
- 3 tiled on a chip.

- 1 31. The method of claim 30, wherein said chip wild-
- 2 type sequence is displayed as a first sequence in said first
- 3 area.
- 1 32. The method of claim 30, further comprising the
- 2 step of displaying a label in said first area to identify said
- 3 chip wild-type sequence.
- 1 33. The method of claim 32, wherein said label is a
- 2 capital C.
- 1 34. The method of claim 27, wherein said at least
- one sample sequence has been hybridized on a chip.
- 1 35. The method of claim 27, further comprising the
- 2 step of indicating bases that differ among a plurality of user
- 3 selected sequences.
- 1 36. The method of claim 27, further comprising the
- 2 steps of:
- displaying a name associated with each of said at
- 4 least one reference sequence in said first area; and
- displaying a name associated with each of said at
- 6 least one sample sequence in said second area.
- 1 37. The method of claim 27, further comprising the
- step of linking at least one reference sequence in said first
- 3 area with at least one sample sequence in said second area.
- 1 38. The method of claim 37, further comprising the
- 2 step of indicating on said display device which sequences are
- 3 linked.
- 1 39. The method of claim 38, wherein said indicating
- step includes the step of displaying a common symbol next to
- 3 said linked sequences.

- 1 40. The method of claim 39, wherein said common 2 symbol is a link number.
- 1 41. The method of claim 37, further comprising the
- 2 step of indicating bases of said at least one sample sequence
- 3 that are not equal to a corresponding base in said at least
- 4 one reference sequence.
- 1 42. The method of claim 27, wherein said at least
- one reference sequence and said at least one sample sequence
- 3 are aligned on said display device.
- 1 43. The method of claim 27, further comprising the
- 2 step of exposing sequences to probes.
- 1 44. The method of claim 43, further comprising the
- 2 step of evaluating said exposed sequences according to
- 3 hybridization with said probes.